



US-108
SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> Inosine producing bacterium belonging to the genus
Bacillus and method for producing inosine

<130> US-108

<150> JP 2003-37760
<151> 2003-02-17

<160> 16

<170> PatentIn Ver. 2.0

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 2
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<220>
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<210> 3
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<212> DNA
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<210> 4
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<210> 5
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33

<210> 10

<211> 33

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33

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<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (259)..(1113)

<400> 11

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agagaattta taacgggtta agaggcttct gcgatcaagt ttatgcggtg agaatgatcg 180
gcgaacagaa cgctcttgat taaatccgta tgtaagtta tattgatctt aaaatattcg 240
gattttgggg gtgagttc atg aag ttt cgt cgc agc ggc aga ttg gtg gac 291
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                1               5               10
tta aca aat tat ttg tta acc cat ccg cac gag tta ata ccg cta acc 339
Leu Thr Asn Tyr Leu Leu Thr His Pro His Glu Leu Ile Pro Leu Thr
                15               20               25
ttt ttc tct gag cgg tat gaa tct gca aaa tca tcg atc agt gaa gat 387
Phe Phe Ser Glu Arg Tyr Glu Ser Ala Lys Ser Ser Ile Ser Glu Asp
                30               35               40
tta aca att att aaa caa acc ttt gaa cag cag ggg att ggt act ttg 435
Leu Thr Ile Ile Lys Gln Thr Phe Glu Gln Gln Gly Ile Gly Thr Leu
                45               50               55
ctt act gtt ccc gga gct gcc gga ggc gtt aaa tat att ccg aaa atg 483
Leu Thr Val Pro Gly Ala Ala Gly Gly Val Lys Tyr Ile Pro Lys Met
                60               65               70               75
aag cag gct gaa gct gaa gag ttt gtg cag aca ctt gga cag tcg ctg 531
Lys Gln Ala Glu Ala Glu Glu Phe Val Gln Thr Leu Gly Gln Ser Leu
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gca aat cct gag cgt atc ctt ccg ggc ggt tat gta tat tta acg gat 579
Ala Asn Pro Glu Arg Ile Leu Pro Gly Gly Tyr Val Tyr Leu Thr Asp
                95               100               105
atc tta gga aag cca tct gta ctc tcc aag gta ggg aag ctg ttt gct 627
Ile Leu Gly Lys Pro Ser Val Leu Ser Lys Val Gly Lys Leu Phe Ala
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Lys	Gly	Ile	Pro	Leu	Ala	Tyr	Ala	Ala	Ala	Ser	Tyr	Leu	Asn	Val	Pro	
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Val	Val	Ile	Val	Arg	Lys	Asp	Asn	Lys	Val	Thr	Glu	Gly	Ser	Thr	Val	
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Ser	Ile	Asn	Tyr	Val	Ser	Gly	Ser	Ser	Asn	Arg	Ile	Gln	Thr	Met	Ser	
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Leu	Ala	Lys	Arg	Ser	Met	Lys	Thr	Gly	Ser	Asn	Val	Leu	Ile	Ile	Asp	
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Asp	Phe	Met	Lys	Ala	Gly	Gly	Thr	Ile	Asn	Gly	Met	Ile	Asn	Leu	Leu	
	205					210					215					
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Asp	Glu	Phe	Asn	Ala	Asn	Val	Ala	Gly	Ile	Gly	Val	Leu	Val	Glu	Ala	
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Glu	Gly	Val	Asp	Glu	Arg	Leu	Val	Asp	Glu	Tyr	Met	Ser	Leu	Leu	Thr	
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Leu	Ser	Thr	Ile	Asn	Met	Lys	Glu	Lys	Ser	Ile	Glu	Ile	Gln	Asn	Gly	
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aat	ttt	ctg	cgt	ttt	ttt	aaa	gac	aat	ctt	tta	aag	aat	gga	gag	aca	1107
Asn	Phe	Leu	Arg	Phe	Phe	Lys	Asp	Asn	Leu	Leu	Lys	Asn	Gly	Glu	Thr	
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gaa	tca	tgacaaaagc	agtcacacaca	aaacatgccc	cagcggcaat	cgggccttat										1163
Glu	Ser															
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<211> 285

<212> PRT

<213> Bacillus subtilis

<400> 12

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Gln	Thr	Phe	Glu	Gln	Gln	Gly	Ile	Gly	Thr	Leu	Leu	Thr	Val	Pro	Gly	
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Glu	Glu	Phe	Val	Gln	Thr	Leu	Gly	Gln	Ser	Leu	Ala	Asn	Pro	Glu	Arg	
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Ile	Leu	Pro	Gly	Gly	Tyr	Val	Tyr	Leu	Thr	Asp	Ile	Leu	Gly	Lys	Pro	
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Ser	Val	Leu	Ser	Lys	Val	Gly	Lys	Leu	Phe	Ala	Ser	Val	Phe	Ala	Glu	

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Arg	Glu	Ile	Asp	Val	Val	Met	Thr	Val	Ala	Thr	Lys	Gly	Ile	Pro	Leu
130		115				135		120			140		125		
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Ser	Gly	Ser	Ser	Asn	Arg	Ile	Gln	Thr	Met	Ser	Leu	Ala	Lys	Arg	Ser
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Arg	Leu	Val	Asp	Glu	Tyr	Met	Ser	Leu	Leu	Thr	Leu	Ser	Thr	Ile	Asn
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<211> 1490

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (101)..(1393)

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gta gta ggt acg caa tgg ggc gat gaa gga aaa ggt aaa att aca gat	163					
Val Val Gly Thr Gln Trp Gly Asp Glu Gly Lys Gly Lys Ile Thr Asp						
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ttc cta tca gaa aat gca gaa gtg atc gcc cgt tat caa ggc gga aat	211					
Phe Leu Ser Glu Asn Ala Glu Val Ile Ala Arg Tyr Gln Gly Gly Asn						
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aac gca ggg cat aca atc aag ttt gac gga atc aca tat aag ctt cac	259					
Asn Ala Gly His Thr Ile Lys Phe Asp Gly Ile Thr Tyr Lys Leu His						
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tta atc ccg tct gga att ttc tat aag gat aaa acg tgt gta atc gga	307					
Leu Ile Pro Ser Gly Ile Phe Tyr Lys Asp Lys Thr Cys Val Ile Gly						
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aac gga atg gtt gta gat ccg aaa gca tta gtc aca gag ctt gcg tat	355					
Asn Gly Met Val Val Asp Pro Lys Ala Leu Val Thr Glu Leu Ala Tyr						
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ctt cat gag cgc aac gtg agt aca gat aac ctg aga atc agc aac aga	403					
Leu His Glu Arg Asn Val Ser Thr Asp Asn Leu Arg Ile Ser Asn Arg						
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gct cac gtc att ctg ccg tat cat ttg aaa ttg gat gaa gtg gaa gaa	451					
	95					
	100					

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Glu	Arg	Lys	Gly	Ala	Asn	Lys	Ile	Gly	Thr	Thr	Lys	Lys	Gly	Ile	Gly
		120					125					130			
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Pro	Ala	Tyr	Met	Asp	Lys	Ala	Ala	Arg	Ile	Gly	Ile	Arg	Ile	Ala	Asp
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Leu	Leu	Asp	Arg	Asp	Ala	Phe	Ala	Glu	Lys	Leu	Glu	Arg	Asn	Leu	Glu
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gaa	aaa	aac	cgt	ctt	ctc	gag	aaa	atg	tac	gag	aca	gaa	ggg	ttt	aaa
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Lys	Tyr	Val	Cys	Asp	Thr	Ser	Val	Val	Leu	Asn	Asp	Ala	Leu	Asp	Glu
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Gly	Arg	Arg	Val	Leu	Phe	Glu	Gly	Ala	Gln	Gly	Val	Met	Leu	Asp	Ile
	215					220					225				
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Asp	Gln	Gly	Thr	Tyr	Pro	Phe	Val	Thr	Ser	Ser	Asn	Pro	Val	Ala	Gly
230					235				240					245	
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Val	Gly	Val	Ser	Lys	Ala	Tyr	Thr	Thr	Arg	Val	Gly	Asp	Gly	Pro	Phe
			265					270					275		
ccg	act	gag	ctg	aaa	gat	gaa	atc	ggc	gat	caa	atc	cgt	gaa	gtc	gga
Pro	Thr	Glu	Leu	Lys	Asp	Glu	Ile	Gly	Asp	Gln	Ile	Arg	Glu	Val	Gly
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Asp	Ser	Val	Val	Val	Arg	His	Ala	Arg	Arg	Val	Ser	Gly	Ile	Thr	Asp
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atc	tgt	gtg	gcg	tac	cgc	tac	aaa	ggc	gaa	atc	att	gaa	gaa	ttc	cca
Ile	Cys	Val	Ala	Tyr	Arg	Tyr	Lys	Gly	Glu	Ile	Ile	Glu	Glu	Phe	Pro
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gca	agt	ctt	aag	gca	ctt	gct	gaa	tgt	gag	ccg	gta	tat	gaa	gaa	atg
Ala	Ser	Leu	Lys	Ala	Leu	Ala	Glu	Cys	Glu	Pro	Val	Tyr	Glu	Glu	Met
		360				365						370			
ccg	ggc	tggt	act	gag	gat	att	aca	ggt	gcg	aag	agc	ttg	agc	gag	ctt
Pro	Gly	Trp	Thr	Glu	Asp	Ile	Thr	Gly	Ala	Lys	Ser	Leu	Ser	Glu	Leu
	375					380					385				
ccg	gaa	aat	gcg	cgc	cat	tat	ctt	gag	cgt	gtg	tct	cag	ctg	aca	ggc
Pro	Glu	Asn	Ala	Arg	His	Tyr	Leu	Glu	Arg	Val	Ser	Gln	Leu	Thr	Gly

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Ile Pro Leu Ser Ile Phe Ser Val Gly Pro Asp Arg Ser Gln Thr Asn
          410          415          420
gtc ctt cgc agt gtg tac cgt gcg aac taa atagaatatg tctgcaagcc 1413
Val Leu Arg Ser Val Tyr Arg Ala Asn
          425          430
cctattttaag gggcttggtt tttgtttgaa agccgcatat aagttggtct gagaaaaaaa 1473
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<210> 14
 <211> 430
 <212> PRT
 <213> *Bacillus subtilis*

<400> 14

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Tyr Gln Gly Gly Asn Asn Ala Gly His Thr Ile Lys Phe Asp Gly Ile
          35          40          45
Thr Tyr Lys Leu His Leu Ile Pro Ser Gly Ile Phe Tyr Lys Asp Lys
          50          55          60
Thr Cys Val Ile Gly Asn Gly Met Val Val Asp Pro Lys Ala Leu Val
          65          70          75          80
Thr Glu Leu Ala Tyr Leu His Glu Arg Asn Val Ser Thr Asp Asn Leu
          85          90          95
Arg Ile Ser Asn Arg Ala His Val Ile Leu Pro Tyr His Leu Lys Leu
          100          105          110
Asp Glu Val Glu Glu Glu Arg Lys Gly Ala Asn Lys Ile Gly Thr Thr
          115          120          125
Lys Lys Gly Ile Gly Pro Ala Tyr Met Asp Lys Ala Ala Arg Ile Gly
          130          135          140
Ile Arg Ile Ala Asp Leu Leu Asp Arg Asp Ala Phe Ala Glu Lys Leu
          145          150          155          160
Glu Arg Asn Leu Glu Glu Lys Asn Arg Leu Leu Glu Lys Met Tyr Glu
          165          170          175          180
Thr Glu Gly Phe Lys Leu Glu Asp Ile Leu Asp Glu Tyr Tyr Glu Tyr
          185          190          195          200
Gly Gln Gln Ile Lys Lys Tyr Val Cys Asp Thr Ser Val Val Leu Asn
          205          210          215          220
Asp Ala Leu Asp Glu Gly Arg Arg Val Leu Phe Glu Gly Ala Gln Gly
          225          230          235          240
Val Met Leu Asp Ile Asp Gln Gly Thr Tyr Pro Phe Val Thr Ser Ser
          245          250          255          260
Asn Pro Val Ala Gly Gly Val Thr Ile Gly Ser Gly Val Gly Pro Thr
          265          270          275          280
Lys Ile Lys His Val Val Gly Val Ser Lys Ala Tyr Thr Thr Arg Val
          285          290          295          300
Gly Asp Gly Pro Phe Pro Thr Glu Leu Lys Asp Glu Ile Gly Asp Gln
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Ile Arg Glu Val Gly Arg Glu Tyr Gly Thr Thr Thr Gly Arg Pro Arg
          325          330          335          340
Arg Val Gly Trp Phe Asp Ser Val Val Val Arg His Ala Arg Arg Val

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Ile	Glu	Glu	Phe	Pro	Ala	Ser	Leu	Lys	Ala	Leu	Ala	Glu	Cys	Glu	Pro		
		355					360					365					
Val	Tyr	Glu	Glu	Met	Pro	Gly	Trp	Thr	Glu	Asp	Ile	Thr	Gly	Ala	Lys		
	370					375					380						
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	385				390					395					400		
Ser	Gln	Leu	Thr	Gly	Ile	Pro	Leu	Ser	Ile	Phe	Ser	Val	Gly	Pro	Asp		
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<220>
 <221> CDS
 <222> (101)..(802)

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 Met Ser Val His Ile 5
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 ggt gct gaa aaa gga caa att gcg gat act gtg ctt ttg ccg gga gat 163
 Gly Ala Glu Lys Gly Gln Ile Ala Asp Thr Val Leu Leu Pro Gly Asp 20
 10
 cct ctc aga gca aaa ttt att gca gaa acg tat ctt gaa aat gta gaa 211
 Pro Leu Arg Ala Lys Phe Ile Ala Glu Thr Tyr Leu Glu Asn Val Glu 35
 25
 tgc tac aat gaa gtc aga ggc atg tat gga ttt acg ggt aca tat aaa 259
 Cys Tyr Asn Glu Val Arg Gly Met Tyr Gly Phe Thr Gly Thr Tyr Lys 50
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 ggt aaa aaa atc tca gta caa ggc acg gga atg gga gtt ccg tct att 307
 Gly Lys Lys Ile Ser Val Gln Gly Thr Gly Met Gly Val Pro Ser Ile 65
 55
 tca att tat gtg aat gaa tta att caa agc tac gat gtg caa aat cta 355
 Ser Ile Tyr Val Asn Glu Leu Ile Gln Ser Tyr Asp Val Gln Asn Leu 85
 70
 ata aga gtc ggt tcc tgc ggc gct att cgt aaa gat gtc aaa gtg cga 403
 Ile Arg Val Gly Ser Cys Gly Ala Ile Arg Lys Asp Val Lys Val Arg 95
 90
 gac gtc att ttg gcg atg acc tcc tca act gat tca caa atg aac aga 451
 Asp Val Ile Leu Ala Met Thr Ser Ser Thr Asp Ser Gln Met Asn Arg 105
 110
 gtt gct ttc gga agc gtt gat ttt gcg cct tgc gca gat ttc gag ctt 499
 Val Ala Phe Gly Ser Val Asp Phe Ala Pro Cys Ala Asp Phe Glu Leu 120
 125
 tta aaa aat gcc tat gat gcc gca aag gat aaa ggt gtg ccg gtg act 547
 130

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Leu	Lys	Asn	Ala	Tyr	Asp	Ala	Ala	Lys	Asp	Lys	Gly	Val	Pro	Val	Thr	
	135					140					145					
gta	gga	agc	gta	ttt	aca	gct	gac	cag	ttc	tac	aat	gac	gat	tcg	caa	595
Val	Gly	Ser	Val	Phe	Thr	Ala	Asp	Gln	Phe	Tyr	Asn	Asp	Asp	Ser	Gln	
150					155					160					165	
att	gaa	aaa	ctt	gca	aaa	tac	ggt	gtg	ctt	ggc	gtt	gaa	atg	gaa	aca	643
Ile	Glu	Lys	Leu	Ala	Lys	Tyr	Gly	Val	Leu	Gly	Val	Glu	Met	Glu	Thr	
				170					175					180		
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Thr	Ala	Leu	Tyr	Thr	Leu	Ala	Ala	Lys	His	Gly	Arg	Lys	Ala	Leu	Ser	
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Ile	Leu	Thr	Val	Ser	Asp	His	Val	Leu	Thr	Gly	Glu	Glu	Thr	Thr	Ala	
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Glu	Glu	Arg	Gln	Thr	Thr	Phe	His	Asp	Met	Ile	Glu	Val	Ala	Leu	His	
	215					220					225					
tcc	gta	tca	caa	taa	aatatatcaa	gaggcgtgct	gggtgccggc	agcctcttct								842
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<211> 233

<212> PRT

<213> Bacillus subtilis

<400> 16

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			100					105					110			
Ser	Gln	Met	Asn	Arg	Val	Ala	Phe	Gly	Ser	Val	Asp	Phe	Ala	Pro	Cys	
	115						120					125				
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			165					170						175		
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			180					185					190			
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